SEQUENCE LISTING

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        E. I. du Pont de Nemours and Company

<120>   GENES FOR DESATURASES TO ALTER LIPID PROFILES IN CORN

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<151>   JUNE 11, 1998

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gag cag gtc gcc cgt gct acc ggc ggt ggc gcg gca gtg cag cgg tcg   274
Glu Gln Val Ala Arg Ala Thr Gly Gly Gly Ala Ala Val Gln Arg Ser
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ccg gtg gag aag ccg ccg ttc acg ttg ggg cag atc aag aag gcg atc   322
Pro Val Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile
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ccg ccg cac tgc ttc gag cgc tcc gtg ctg agg tcc ttc tcg tac gtg   370
Pro Pro His Cys Phe Glu Arg Ser Val Leu Arg Ser Phe Ser Tyr Val
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gcc cac gac ctg gcg ctc gcc gcg gcg ctc ctc tac ctc gcg gtg gcc   418
Ala His Asp Leu Ala Leu Ala Ala Ala Leu Leu Tyr Leu Ala Val Ala
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gtg ata ccg gcg cta ccc tgc ccg ctc cgc tac gcg gcc tgg ccg ctg   466
Val Ile Pro Ala Leu Pro Cys Pro Leu Arg Tyr Ala Ala Trp Pro Leu
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tac tgg gtg gcc cag ggg tgc gtg tgc acg ggc gtg tgg gtg atc gcg   514
Tyr Trp Val Ala Gln Gly Cys Val Cys Thr Gly Val Trp Val Ile Ala
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cac gag tgc ggc cac cac gcc ttc tcc gac cac gcg ctc ctg gac gac   562
His Glu Cys Gly His His Ala Phe Ser Asp His Ala Leu Leu Asp Asp
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gcc gtc ggc ctg gcg ctg cac tcg gcg ctg ctg gtg ccc tac ttc tcg   610
Ala Val Gly Leu Ala Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser
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Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu
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cgc gac gag gtg ttc gtg ccg agg acc aag gag gcg ctg ccg tgg tac   706
Arg Asp Glu Val Phe Val Pro Arg Thr Lys Glu Ala Leu Pro Trp Tyr
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gcc ccg tac gtg cac ggc agc ccc gcg ggc cgg ctg gcg cac gtc gcc   754
Ala Pro Tyr Val His Gly Ser Pro Ala Gly Arg Leu Ala His Val Ala
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gtg cag ctc acc ctg ggc tgg ccg ctg tac ctg gcc acc aac gcg tcg   802
Val Gln Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser
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Gly Arg Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro
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2

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Val Ala Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly
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ctc tgg tgg gtg gtg cgc gtg tac gcc gtg ccg ctg ctg atc gtc aac         994
Leu Trp Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn
            260                 265                 270

gcg tgg ctg gtg ctc atc acg tac ctg cag cac acc cac ccg gcg ctg        1042
Ala Trp Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ala Leu
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ccc cac tac gac tcg ggc gag tgg gac tgg ctg cgc ggc gcg ctc gcc        1090
Pro His Tyr Asp Ser Gly Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala
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acc gtc gac cgc gac tac ggc gtc ctc aac cgc gtg ttc cac cac atc        1138
Thr Val Asp Arg Asp Tyr Gly Val Leu Asn Arg Val Phe His His Ile
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acg gac acg cac gtc gcg cac cac ctc ttc tcc acc atg ccg cac tac        1186
Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr
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His Ala Val Glu Ala Thr Arg Ala Ile Arg Pro Val Leu Gly Glu Tyr
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Tyr Gln Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala
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agg gag tgc atc tac gtc gag cct gag aac cgc aac cgc aag ggc gtc        1330
Arg Glu Cys Ile Tyr Val Glu Pro Glu Asn Arg Asn Arg Lys Gly Val
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Phe Trp Tyr Asn Ser Lys Phe
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Ser Pro Val Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala
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3

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Ile Pro Pro His Cys Phe Glu Arg Ser Val Leu Arg Ser Phe Ser Tyr
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Val Ala His Asp Leu Ala Leu Ala Ala Ala Leu Leu Tyr Leu Ala Val
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Ala Val Ile Pro Ala Leu Pro Cys Pro Leu Arg Tyr Ala Ala Trp Pro
85              90              95

Leu Tyr Trp Val Ala Gln Gly Cys Val Cys Thr Gly Val Trp Val Ile
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Ala His Glu Cys Gly His His Ala Phe Ser Asp His Ala Leu Leu Asp
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Asp Ala Val Gly Leu Ala Leu His Ser Ala Leu Leu Val Pro Tyr Phe
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Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu
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Glu Arg Asp Glu Val Phe Val Pro Arg Thr Lys Glu Ala Leu Pro Trp
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Tyr Ala Pro Tyr Val His Gly Ser Pro Ala Gly Arg Leu Ala His Val
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Ala Val Gln Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala
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Ser Gly Arg Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly
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Pro Ile Tyr Gly Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala
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Gly Val Ala Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe
245             250             255

Gly Leu Trp Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val
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Leu Pro His Tyr Asp Ser Gly Glu Trp Asp Trp Leu Arg Gly Ala Leu
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Ala Thr Val Asp Arg Asp Tyr Gly Val Leu Asn Arg Val Phe His His
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Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His
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Tyr His Ala Val Glu Ala Thr Arg Ala Ile Arg Pro Val Leu Gly Glu
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Tyr Tyr Gln Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu
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6

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7

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<213>  Zea mays

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8

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<220>
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attggcctcc ggg atg gcg ctc cgc ctc cac gac gtc gcg ctc tgc ctc    169

        Met Ala Leu Arg Leu His Asp Val Ala Leu Cys Leu
         1               5                  10

tcc ccg ccg ctc gcc gcc cgc cgc cgc agc ggc ggc agt ttc gtc gcc    217
Ser Pro Pro Leu Ala Ala Arg Arg Arg Ser Gly Gly Ser Phe Val Ala
        15                  20                  25

gtc gcc tcc atg acg tcc gcc gcc gtc tcc acc agg gtg gag aac aag    265
Val Ala Ser Met Thr Ser Ala Ala Val Ser Thr Arg Val Glu Asn Lys
    30                  35                  40

aag cca ttt gct cct ccg agg gag gta cat gtc cag gtt aca cat tca    313
Lys Pro Phe Ala Pro Pro Arg Glu Val His Val Gln Val Thr His Ser
```

9

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atg cca tct cac aag att gaa att ttc aag tca ctt gat gat tgg gct   361
Met Pro Ser His Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala
                 65                  70                  75

aga gat aat atc ttg aca cat ctc aag cca gtc gag aag tgt tgg cag   409
Arg Asp Asn Ile Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln
                 80                  85                  90

cca cag gat ttc ctc cct gac cca gca tct gaa gga ttt cat gat gaa   457
Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu
                 95                 100                 105

gtt aag gag ctc aga gaa cgt gcc aag gag atc cct gat gat tat ttt   505
Val Lys Glu Leu Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe
        110                 115                 120

gtt tgt ttg gtt gga gac atg att act gag gaa gct cta cca aca tac   553
Val Cys Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
125                 130                 135                 140

cag act atg ctt aac acc ctc gac ggt gtc aga gat gag aca ggt gca   601
Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
                145                 150                 155

agc ccc act gct tgg gct gtt tgg acg agg gca tgg act gct gag gag   649
Ser Pro Thr Ala Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu
                160                 165                 170

aac agg cat ggt gat ctt ctc aac aag tac atg tac ctc act ggg agg   697
Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg
                175                 180                 185

gta gat atc agg caa att gag aag aca att cag tat ctt att ggc tct   745
Val Asp Ile Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser
        190                 195                 200

gga atg gat cct agg act gag aat aat cct tat ctt ggt ttc gtc tac   793
Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Val Tyr
205                 210                 215                 220

acc tcc ttc caa gag cgg gcg acc ttc atc tcg cat ggg aac act gct   841
Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala
                225                 230                 235
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10

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Arg His Ala Lys Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly
            240                 245                 250

atc atc gcc tca gat gag aag cga cat gaa act gcg tac acc aag atc    937
Ile Ile Ala Ser Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
            255                 260                 265

gtg gag aag ttg ttt gag atc gac cct gat ggt aca gtg gtt gct ctg    985
Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu
        270                 275                 280

gct gac atg atg aag aag aag atc tca atg cct gcc cac ctg atg ttt   1033
Ala Asp Met Met Lys Lys Lys Ile Ser Met Pro Ala His Leu Met Phe
285                 290                 295                 300

gac ggt cag gac gac aag ctg ttt gag cac ttc tcc atg gtc gcg cag   1081
Asp Gly Gln Asp Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln
                305                 310                 315

agg ctt ggc gtt tac acc gcc agg gac tac gcc gac att ctt gag ttc   1129
Arg Leu Gly Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe
            320                 325                 330

ctt gtt gac agg tgg aag gtg gcg gac ctg act ggt ctg tcg ggt gag   1177
Leu Val Asp Arg Trp Lys Val Ala Asp Leu Thr Gly Leu Ser Gly Glu
            335                 340                 345

ggg aac aag gcg cag gac tac ctc tgc acc ctt gct tca agg atc cgg   1225
Gly Asn Lys Ala Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg
        350                 355                 360

agg cta gac gag agg gcc cag agc aga gcc aag aaa gca ggc acg ctg   1273
Arg Leu Asp Glu Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu
365                 370                 375                 380

cct ttc agc tgg gta tat ggt agg gaa gtc caa ctg tga aatcggaaac   1322
Pro Phe Ser Trp Val Tyr Gly Arg Glu Val Gln Leu
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<212> PRT
<213> Zea mays

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Thr Ser Ala Ala Val Ser Thr Arg Val Glu Asn Lys Lys Pro Phe Ala
            35                  40                  45

Pro Pro Arg Glu Val His Val Gln Val Thr His Ser Met Pro Ser His
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11

```
              50                    55                    60
Lys Ile Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asp Asn Ile
65                  70                  75                  80

Leu Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp Phe
                85                  90                  95

Leu Pro Asp Pro Ala Ser Glu Gly Phe His Asp Glu Val Lys Glu Leu
            100                 105                 110

Arg Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Cys Leu Val
            115                 120                 125

Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu
        130                 135                 140

Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr Ala
145                 150                 155                 160

Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly
            165                 170                 175

Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val Asp Ile Arg
            180                 185                 190

Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro
        195                 200                 205

Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Val Tyr Thr Ser Phe Gln
    210                 215                 220

Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg His Ala Lys
225                 230                 235                 240

Asp Phe Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Ile Ile Ala Ser
            245                 250                 255

Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu
            260                 265                 270

Phe Glu Ile Asp Pro Asp Gly Thr Val Val Ala Leu Ala Asp Met Met
    275                 280                 285

Lys Lys Lys Ile Ser Met Pro Ala His Leu Met Phe Asp Gly Gln Asp
290                 295                 300

Asp Lys Leu Phe Glu His Phe Ser Met Val Ala Gln Arg Leu Gly Val
305                 310                 315                 320

Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Asp Arg
            325                 330                 335

Trp Lys Val Ala Asp Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys Ala
        340                 345                 350

Gln Asp Tyr Leu Cys Thr Leu Ala Ser Arg Ile Arg Arg Leu Asp Glu
        355                 360                 365

Arg Ala Gln Ser Arg Ala Lys Lys Ala Gly Thr Leu Pro Phe Ser Trp
370                 375                 380

Val Tyr Gly Arg Glu Val Gln Leu
385                 390
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12

<210> 10
<211> 1709
<212> DNA
<213> Zea mays

<220>
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gtcgagatct tgccgaggc ggtgaccgtc gagggatcgc c atg gcg ttg agg gcg   116
                                             Met Ala Leu Arg Ala
                                             1   5

tcc ccc gtg tcg cat ggc acc gcg gca gcg ccg ctg ccg cct ttc gcg   164
Ser Pro Val Ser His Gly Thr Ala Ala Ala Pro Leu Pro Pro Phe Ala
                10   15   20

cgg agg aag atg gcc cgt ggg gtg gtg gtg gcc atg gcg tcc acc atc   212
Arg Arg Lys Met Ala Arg Gly Val Val Val Ala Met Ala Ser Thr Ile
            25   30   35

aac agg gtc aaa act gtc aaa gaa ccc tat acc cct cca cga gag gta   260
Asn Arg Val Lys Thr Val Lys Glu Pro Tyr Thr Pro Pro Arg Glu Val
        40   45   50

cat cgc caa att acc cat tca cta cca cct caa aag cgg gag att ttc   308
His Arg Gln Ile Thr His Ser Leu Pro Pro Gln Lys Arg Glu Ile Phe
    55   60   65

gat tca ctt caa cct tgg gcc aag gat aac cta ctg aac cta ctg aag   356
Asp Ser Leu Gln Pro Trp Ala Lys Asp Asn Leu Leu Asn Leu Leu Lys
70   75   80   85

cca gtt gaa aag tca tgg cag cca cag gac ttc cta cca gag cct tct   404
Pro Val Glu Lys Ser Trp Gln Pro Gln Asp Phe Leu Pro Glu Pro Ser
                90   95   100

tct gat ggg ttt tat gat gaa gtt aaa gaa ctg agg gag cgg gca aat   452
Ser Asp Gly Phe Tyr Asp Glu Val Lys Glu Leu Arg Glu Arg Ala Asn
            105   110   115

gaa ata cct gat gaa tac ttt gtt tgc tta gtt ggt gat atg gtt act   500
Glu Ile Pro Asp Glu Tyr Phe Val Cys Leu Val Gly Asp Met Val Thr
            120   125   130

gag gaa gcc tta cct aca tac caa aca atg ctt aac act ctt gat gga   548
Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly
            135   140   145

gtc cgg gat gaa act ggt gca agt tca acc acg tgg gcg gtt tgg aca   596
Val Arg Asp Glu Thr Gly Ala Ser Ser Thr Thr Trp Ala Val Trp Thr
150   155   160   165

agg gca tgg aca gct gaa gag aac aga cat ggt gac ctc ctt aac aag   644
Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys
                170   175   180

tac atg tac ctt act gga cgg gtt gac atg aaa caa att gag aag acc   692
Tyr Met Tyr Leu Thr Gly Arg Val Asp Met Lys Gln Ile Glu Lys Thr
            185   190   195

13

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ata caa tat ctg att ggt tcc gga atg gat cct gga act gag aac aac    740
Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro Gly Thr Glu Asn Asn
        200             205             210

ccc tac ttg ggt ttc ctc tac aca tca ttc caa gaa agg gca aca ttt    788
Pro Tyr Leu Gly Phe Leu Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe
        215             220             225

gtg tcg cat ggg aat act gca agg cat gcc aag gag tat ggt gat ctc    836
Val Ser His Gly Asn Thr Ala Arg His Ala Lys Glu Tyr Gly Asp Leu
230             235             240             245

aag ctg gcc cag ata tgt ggc acg ata gca gcc gat gag aag cgc cac    884
Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His
            250             255             260

gaa aca gcc tac acc aag ata gtc gag aag ctc ttc gag atg gac cct    932
Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Met Asp Pro
                265             270             275

gat tac aca gtg ctt gcg ttt gct gac atg atg agg aag aag atc acg    980
Asp Tyr Thr Val Leu Ala Phe Ala Asp Met Met Arg Lys Lys Ile Thr
            280             285             290

atg cca gcc cat ctc atg tac gac ggt aag gac gac aac ctg ttc gag   1028
Met Pro Ala His Leu Met Tyr Asp Gly Lys Asp Asp Asn Leu Phe Glu
        295             300             305

cac ttc agc gcg gtg gcg cag agg ctg ggc gtc tac acc gcc aaa gac   1076
His Phe Ser Ala Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Lys Asp
310             315             320             325

tac gcc gac atc ctc gag ttc ctg gtc cag agg tgg aaa gtc gcg gag   1124
Tyr Ala Asp Ile Leu Glu Phe Leu Val Gln Arg Trp Lys Val Ala Glu
            330             335             340

ctc aca ggg ctg tct gga gaa ggg aga agc gcg cag gac ttt gtc tgt   1172
Leu Thr Gly Leu Ser Gly Glu Gly Arg Ser Ala Gln Asp Phe Val Cys
            345             350             355

acc ttg gcg ccg agg atc agg cgg ctg gat gat aga gct caa gcg agg   1220
Thr Leu Ala Pro Arg Ile Arg Arg Leu Asp Asp Arg Ala Gln Ala Arg
            360             365             370

gcg aag caa gca ccg gtt att cct ttc agt tgg gtt tat gac cgc aag   1268
Ala Lys Gln Ala Pro Val Ile Pro Phe Ser Trp Val Tyr Asp Arg Lys
        375             380             385

gtg cag ctt taa tcaagaacgc taggcaatgt gggcatttac tacgtatatc      1320
Val Gln Leu
390

attttcagtc ctggggttct ctataagaaa cagtctctag gttatctagc agggtagaat 1380
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<210>   11
<211>   392
<212>   PRT
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14

<213> Zea mays

<400> 11

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 1   5   10   15

Leu Pro Pro Phe Ala Arg Arg Lys Met Ala Arg Gly Val Val Val Ala
            20   25   30

Met Ala Ser Thr Ile Asn Arg Val Lys Thr Val Lys Glu Pro Tyr Thr
        35   40   45

Pro Pro Arg Glu Val His Arg Gln Ile Thr His Ser Leu Pro Pro Gln
    50   55   60

Lys Arg Glu Ile Phe Asp Ser Leu Gln Pro Trp Ala Lys Asp Asn Leu
65   70   75   80

Leu Asn Leu Leu Lys Pro Val Glu Lys Ser Trp Gln Pro Gln Asp Phe
            85   90   95

Leu Pro Glu Pro Ser Ser Asp Gly Phe Tyr Asp Glu Val Lys Glu Leu
            100   105   110

Arg Glu Arg Ala Asn Glu Ile Pro Asp Glu Tyr Phe Val Cys Leu Val
        115   120   125

Gly Asp Met Val Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu
    130   135   140

Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Ser Thr Thr
145   150   155   160

Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly
            165   170   175

Asp Leu Leu Asn Lys Tyr Met Tyr Leu Thr Gly Arg Val Asp Met Lys
            180   185   190

Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro
    195   200   205

Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe Leu Tyr Thr Ser Phe Gln
    210   215   220

Glu Arg Ala Thr Phe Val Ser His Gly Asn Thr Ala Arg His Ala Lys
225   230   235   240

Glu Tyr Gly Asp Leu Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala
            245   250   255

Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu
            260   265   270

Phe Glu Met Asp Pro Asp Tyr Thr Val Leu Ala Phe Ala Asp Met Met
    275   280   285

Arg Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Lys Asp
    290   295   300

Asp Asn Leu Phe Glu His Phe Ser Ala Val Ala Gln Arg Leu Gly Val
305   310   315   320

Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gln Arg

15

Trp Lys Val Ala Glu Leu Thr Gly Leu Ser Gly Glu Gly Arg Ser Ala
        340   345   350

Gln Asp Phe Val Cys Thr Leu Ala Pro Arg Ile Arg Arg Leu Asp Asp
        355   360   365

Arg Ala Gln Ala Arg Ala Lys Gln Ala Pro Val Ile Pro Phe Ser Trp
    370   375   380

Val Tyr Asp Arg Lys Val Gln Leu
385   390

<210>   12
<211>   18
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

<400>   12
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<210>   13
<211>   17
<212>   DNA
<213>   Artificial Sequence

<220>
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<400>   13
gcgatggcac tgcagta   17

<210>   14
<211>   21
<212>   DNA
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<220>
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<400>   14
cttgagagaa gaaccacact c   21

<210>   15
<211>   21
<212>   DNA
<213>   Artificial Sequence

<220>
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<400>   15
ctagacatat cgagcatgct g   21

<210>   16
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>

16

<400> 16
aggcgctgac ggtggcgacg ct   22

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 17
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<210> 18
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

<400> 18
acctcccgtc gcaccccggt ggtgatcagc catggtaggc tagcag   46

<210> 19
<211> 1714
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

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ttagctccgt catgaattta gtaaccgact cgatatgtac cgtggaaccc ctagggcatg 180
agccatagga tcatcatatc caaacatgca ccaacaaatc caccacacat cgaagatcca 240
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cacaggggag cttcatatca gatggagcca ttgaattgat ataaaaagct gaagttctaa 360
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gagagataca tacacgacac gttagggacg taaaatgacg gaattataca gctacctcta 480
tatgtgacac ttatgtaata gaaaagacag aatccatatg aagatgtata atggatcaat 540
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17

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gctcgctctg ctagcctacc atggtacgtg gcat                                    1714

<210>   20
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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

<400>   20
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<210>   21
<211>   33
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

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gaggagtgag gatcctgatt gactatctca ttc                                        33

<210>   22
<211>   33
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

<400>   22
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<210>   23
<211>   32
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

<400>   23
agagttggat ccgtgtacaa cttggtctct gg                                         32

<210>   24
<211>   37
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

<400>   24
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<210>   25
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<220>
<223>   Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE
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18

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<400>  25
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<210>  26
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<220>
<223>  Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

<400>  26
gtggcggggc cgaatctcga gtgggccgta gt                          32

<210>  27
<211>  33
<212>  DNA
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<220>
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<400>  27
gccacgtgcc atggtaggct agcagagcga gct                         33

<210>  28
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

<400>  28
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<210>  29
<211>  19
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:  SYNTHETIC OLIGONUCLEOTIDE

<400>  29
ggtctgactt acgggtgtc                                         19

<210>  30
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<212>  DNA
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<220>
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<210>  31
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<220>
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<400> 31
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<210> 32
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

<400> 32
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<210> 33
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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<210> 34
<211> 30
<212> DNA
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<220>
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<400> 34
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<210> 35
<211> 30
<212> DNA
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<220>
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<400> 35
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<210> 36
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

<400> 36
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<210> 37
<211> 39
<212> DNA

<220>
<223> Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

<400> 37
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<210> 38
<211> 1108
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

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ggtggcatga ctacattcca catattagta ctaagcaact aactttgagg aatgaggtga   180
tgatgaatta actcactcca ttccacaaac caaacaaaaa tttgaggagt gagaagatga   240
ttgactatct cattcctcaa accaaacacc tcaaatatat ctgctatcgg gattggcatt   300
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gaagattatt gttgtcttgt ctttcatcat atatcgagtc tttccctagg atattattat   420
tggcaatgag cattacacgg ttaatcgatt gagagaacat gcatctcacc ttcagcaaat   480
aattacgata atccatattt tacgcttcgt aacttctcat gagtttcgat atacaaattt   540
gttttctgga caccctacca ttcatcctct tcggagaaga gaggaagtgt cctcaattta   600
aatatgttgt catgctgtag ttcttcacaa aatctcaaca ggtaccaagc acattgtttc   660
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<210> 39
<211> 871
<212> DNA
<213> Zea mays

<400> 39
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ggcgaagatt attgttgtct tgtctttcat catatatcga gtctttccct aggatattat   180
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tttgtttttct ggacaccta ccattcatcc tcttcggaga agagaggaag tgtcctcaat   360
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agaaaatagt gagacacgga agacaaaaga agtaaaagag gcccggacta cggcccacat   600
gagattcggc cccgccacct ccggcaacca gcggccgatc caacggcagt gcgcgcacac   660
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cacccctac acaggtgtcg cgctgccccc gacacgagtc ccgcatgcgt cccacgcggc   780
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<210> 40
<211> 545
<212> DNA
<213> Zea mays

21

<400> 40

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taaatctata ttattattaa tatactaaaa ctatactgac gctcagatgc ttttactagt  180
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aagaagtaaa agaggcccgg actacggccc acatgagatt cggccccgcc acctccggca  300
accagcggcc gatccaacgg cagtgcgcgc acacacacaa cctcgtatat atcgccgcgc  360
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ccccgacacg agtcccgcat gcgtcccacg cggccgcgcc agatcccgcc tccgcgcgtt  480
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agctc                                                              545
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<210> 41
<211> 952
<212> DNA
<213> Zea mays

<400> 41

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attcctgtat ccctacgccc gtgtaccccc tgtttagaga acctcccaaa gggtataagat  120
ggcgaagatt attgttgtct tgtctttcat catatatcga gtctttccct aggatattat  180
tattggcaat gagcattaca cggttaatcg attgagagaa catgcatctc accttcagca  240
aataattacg ataatccata ttttacgctt cgtaacttct catgagtttc gatatacaaa  300
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<400> 42

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<212>   DNA
<213>   Zea mays

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23

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<400> 49
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<210> 50
<211> 29
<212> DNA
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<220>
<223> Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE

<400> 50
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<210> 51
<211> 29
<212> DNA
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<400> 51
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<210> 52
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<400> 52
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<210> 53
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<210> 57
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26

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27

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